



1600

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/471,459A

DATE: 06/14/2002  
TIME: 14:50:24

Input Set : A:\PC10315A Sequence Listing.ST25.txt  
Output Set: N:\CRF3\06142002\I471459A.raw

ENTERED

3 <110> APPLICANT: Pfizer Inc.  
4 Fidock, Mark David  
6 <120> TITLE OF INVENTION: Enzyme PDE xiv  
8 <130> FILE REFERENCE: PC10315AGPR  
10 <140> CURRENT APPLICATION NUMBER: 09/471,459A  
11 <141> CURRENT FILING DATE: 1999-12-22  
13 <150> PRIOR APPLICATION NUMBER: GB 9828603.2  
14 <151> PRIOR FILING DATE: 1998-12-23  
16 <150> PRIOR APPLICATION NUMBER: GB 9922123.6  
17 <151> PRIOR FILING DATE: 1999-09-17  
19 <160> NUMBER OF SEQ ID NOS: 26  
21 <170> SOFTWARE: PatentIn version 3.1  
23 <210> SEQ ID NO: 1  
24 <211> LENGTH: 446  
25 <212> TYPE: PRT  
26 <213> ORGANISM: Mouse  
28 <400> SEQUENCE: 1  
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34 Pro Glu Gln Ser Val Lys Cys Val Cys Met Leu Gly Asp Val Arg Leu  
35 20 25 30  
38 Arg Gly Gln Thr Gly Val Pro Ala Glu Arg Arg Gly Ser Tyr Pro Phe  
39 35 40 45  
42 Ile Asp Phe Arg Leu Leu Asn Asn Thr Thr His Ser Gly Glu Ile Gly  
43 50 55 60  
46 Thr Lys Lys Lys Val Lys Arg Leu Leu Ser Phe Gln Arg Tyr Phe His  
47 65 70 75 80  
50 Ala Ser Arg Leu Leu Arg Gly Ile Ile Pro Gln Ala Pro Leu His Leu  
51 85 90 95  
54 Leu Asp Glu Asp Tyr Leu Gly Gln Ala Arg His Met Leu Ser Lys Val  
55 100 105 110  
58 Gly Thr Trp Asp Phe Asp Ile Phe Leu Phe Asp Arg Leu Thr Asn Gly  
59 115 120 125  
62 Asn Ser Leu Val Thr Leu Leu Cys His Leu Phe Asn Ser His Gly Leu  
63 130 135 140  
66 Ile His His Phe Lys Leu Asp Met Val Thr Leu His Arg Phe Leu Val  
67 145 150 155 160  
70 Met Val Gln Glu Asp Tyr His Gly His Asn Pro Tyr His Asn Ala Val  
71 165 170 175  
74 His Ala Ala Asp Val Thr Gln Ala Met His Cys Tyr Leu Lys Glu Pro  
75 180 185 190  
78 Lys Leu Ala Ser Phe Leu Thr Pro Leu Asp Ile Met Leu Gly Leu Leu  
79 195 200 205

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82 Ala Ala Ala Ala His Asp Val Asp His Pro Gly Val Asn Gln Pro Phe  
 83 210 215 220  
 86 Leu Ile Lys Thr Asn His His Leu Ala Asn Leu Tyr Gln Asn Met Ser  
 87 225 230 235 240  
 90 Val Leu Glu Asn His His Trp Arg Ser Thr Ile Gly Met Leu Arg Glu  
 91 245 250 255  
 94 Ser Arg Leu Leu Ala His Leu Pro Lys Glu Met Thr Gln Asp Ile Glu  
 95 260 265 270  
 98 Gln Gln Leu Gly Ser Leu Ile Leu Ala Thr Asp Ile Asn Arg Gln Asn  
 99 275 280 285  
 102 Glu Phe Leu Thr Arg Leu Lys Ala His Leu His Asn Lys Asp Leu Arg  
 103 290 295 300  
 106 Leu Glu Asn Val Gln Asp Arg His Phe Met Leu Gln Ile Ala Leu Lys  
 107 305 310 315 320  
 110 Cys Ala Asp Ile Cys Asn Pro Cys Arg Ile Trp Glu Met Ser Lys Gln  
 111 325 330 335  
 114 Trp Ser Glu Arg Val Cys Glu Glu Phe Tyr Arg Gln Gly Asp Leu Glu  
 115 340 345 350  
 118 Gln Lys Phe Glu Leu Glu Ile Ser Pro Leu Cys Asn Gln Gln Lys Asp  
 119 355 360 365  
 122 Ser Ile Pro Ser Ile Gln Ile Gly Phe Met Thr Tyr Ile Val Glu Pro  
 123 370 375 380  
 126 Leu Phe Arg Glu Trp Ala Arg Phe Thr Gly Asn Ser Thr Leu Ser Glu  
 127 385 390 395 400  
 130 Asn Met Leu Ser His Leu Ala His Asn Lys Ala Gln Trp Lys Ser Leu  
 131 405 410 415  
 134 Leu Ser Asn Gln His Arg Arg Gly Ser Gly Gln Asp Leu Ala Gly  
 135 420 425 430  
 138 Pro Ala Pro Glu Thr Leu Glu Gln Thr Glu Gly Ala Thr Pro  
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 143 <211> LENGTH: 1341  
 144 <212> TYPE: DNA  
 145 <213> ORGANISM: Mouse  
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 150 gtc当地atgtt tttgc当地gtct aggagatgtt cgtactaaggg gtc当地agcggg gg当地tccctgcc 120  
 152 gaacgccc当地gtt gctcc当地taccc attc当地tgc当地tccctgtctac ttaacaatata aacacaactca 180  
 154 ggg当地aaatgg gc当地ccaagaa aaaggtgaaa cgtactttaa gtttccaaag atacttccat 240  
 156 gcatcttaggc ttctccgggg gattataccg caggccc当地tcc cccactgtct ggatgaagac 300  
 158 taccttggac aagcaaggca catgctctcc aaagttggaa cgtgggactt tgacattttc 360  
 160 ttgtttgatc gcttgc当地aaa tgggacactg ctggtaactc ttttgc当地tca cctcttcaac 420  
 162 tcccatgggc tcatccacca tttcaagctc gatatggtga cttgc当地cag gtttctggtt 480  
 164 atgggttcagg aagattacca cggtc当地acaac cc当地taccaca atgctgttca cgc当地ccgac 540  
 166 gtc当地ccagg ccatgc当地ctg ttacctgaaag gagccaaatgt tggcaagctt cctcacacct 600  
 168 ctggacatca tgcttggact actggctgca gc当地gctcatg acgtggacca cccaggggtc 660  
 170 aaccagccat ttttgc当地aaa aactaaccac catcttgc当地a acctgtatca gaatatgtct 720  
 172 gtactggaga atc当地ccactg gcgatctaca attggcatgc tt当地gagaatc acggctccctg 780  
 174 gtc当地acttgc caaaggaaat gacacaggat atc当地aacagc agctgggctc cctcatcttgc 840

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176 gccacggata tcaacagaca gaatgagttt ctgaccgcgt taaaagctca cctccacaat 900  
 178 aaagatttga gactggagaa tgtacaggac agacacttta tgcttcagat cgcccttgaag 960  
 180 tgtgctgaca tttgcatacc ttgtcgatcc tgggagatga gcaaggcgtg gagtgaaagg 1020  
 182 gtctgtgagg aattctacag acaagggtgac cttgaacaga agtttgaact ggaaatcagt 1080  
 184 cctctttgtat atcaacagaa agattcaatc cctagcatac aaattggttt catgacttac 1140  
 186 atcgtggaggc cgctgttccg ggagtggggc cggttactg ggaacacgac cctgtcggag 1200  
 188 aacatgctaa gccatctcgc gcacaacaaa gcccagtgga agagcctgct gtccaatcag 1260  
 190 cacagacgca ggggcagcgg ccaggacctg gcgggccccg cacctgagac cctggagcag 1320  
 192 acagaaggtg ccacgcccata a 1341  
 195 <210> SEQ ID NO: 3  
 196 <211> LENGTH: 288  
 197 <212> TYPE: PRT  
 198 <213> ORGANISM: Human  
 200 <400> SEQUENCE: 3  
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 203 1 5 10 15  
 206 Pro Asp Gln Asn Ala Lys Cys Val Cys Met Leu Gly Asp Ile Arg Leu  
 207 20 25 30  
 210 Arg Gly Gln Thr Gly Val Arg Ala Glu Arg Arg Gly Ser Tyr Pro Phe  
 211 35 40 45  
 214 Ile Asp Phe Arg Leu Leu Asn Ser Thr Thr Tyr Ser Gly Glu Ile Gly  
 215 50 55 60  
 218 Thr Lys Lys Lys Val Lys Arg Leu Leu Ser Phe Gln Arg Tyr Phe His  
 219 65 70 75 80  
 222 Ala Ser Arg Leu Leu Arg Gly Ile Ile Pro Gln Ala Pro Leu His Leu  
 223 85 90 95  
 226 Leu Asp Glu Asp Tyr Leu Gly Gln Ala Arg His Met Leu Ser Lys Val  
 227 100 105 110  
 230 Gly Met Trp Asp Phe Asp Ile Phe Leu Phe Asp Arg Leu Thr Asn Gly  
 231 115 120 125  
 234 Asn Ser Leu Val Thr Leu Leu Cys His Leu Phe Asn Thr His Gly Leu  
 235 130 135 140  
 238 Ile His His Phe Lys Leu Asp Met Val Thr Leu His Arg Phe Leu Val  
 239 145 150 155 160  
 242 Met Val Gln Glu Asp Tyr His Ser Gln Asn Pro Tyr His Asn Ala Val  
 243 165 170 175  
 246 His Ala Ala Asp Val Thr Gln Ala Met His Cys Tyr Leu Lys Glu Pro  
 247 180 185 190  
 250 Lys Leu Ala Ser Phe Leu Thr Pro Leu Asp Ile Met Leu Gly Leu Leu  
 251 195 200 205  
 254 Ala Ala Ala His Asp Val Asp His Pro Gly Val Asn Gln Pro Phe  
 255 210 215 220  
 258 Leu Ile Lys Thr Asn His His Leu Ala Asn Leu Tyr Gln Asn Met Ser  
 259 225 230 235 240  
 262 Val Leu Glu Asn His His Trp Arg Ser Thr Ile Gly Met Leu Arg Glu  
 263 245 250 255  
 266 Ser Arg Leu Leu Ala His Leu Pro Lys Glu Met Thr Gly Thr Trp Asp  
 267 260 265 270  
 270 Phe Asp Ile Phe Leu Phe Asp Arg Leu Thr Asn Gly Asn Ser Leu Val

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277	<213> ORGANISM: Human		
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282	gccaaatgtg tttgcacatgtc gggagatata cgactaaggc gtcagacggg ggttcgtgt	120	
284	gaacgcctgt gctccttaccc attcattgtac ttccgcctac ttaacagttac aacatactca	180	
286	ggggagattt gcaccaagaa aaaggtgaaa agactattaa gcttcaaag atacttccat	240	
288	gcaccaaggc tgcttgcgtgg aattatacca caagccccctc tgccacctgtc ggatgaagac	300	
290	taccttggac aagcaaggc tatgctctcc aaagtggaa tggggattt tgacattttc	360	
292	ttgtttgatc gcttgcacaaa tggaaacagc ctggtaacac tgggtgtgcca cctcttcaat	420	
294	acccatggac tcatttacca tttcaagttt gatatggta ctttacaccg atttttagtc	480	
296	atgggtcaag aagattacca cagccaaaac ccgtatcaca atgctgttca cgccggcgcac	540	
298	gtcaccggcagg ccatgcactg ctacctgaaa gagccaaagc ttggcagctt ctcacgcct	600	
300	ctggacatca tgcttggact gctggctgca gcagcacacg atgtggacca cccagggtg	660	
302	aaccagccat ttttgcataaa aactaaccac catcttgcac acctatataca gaatatgtct	720	
304	gtgctggaga atcatcactg gcgatctaca attggcatgc ttggagaatc aaggcttctt	780	
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311	<212> TYPE: PRT		
312	<213> ORGANISM: Human		
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320	Pro Asp Gln Asn Ala Lys Cys Val Cys Met Leu Gly Asp Ile Arg Leu		
321	20 25 30		
324	Arg Gly Gln Thr Gly Val Arg Ala Glu Arg Arg Gly Ser Tyr Pro Phe		
325	35 40 45		
328	Ile Asp Phe Arg Leu Leu Asn Ser Thr Thr Tyr Ser Gly Glu Ile Gly		
329	50 55 60		
332	Thr Lys Lys Lys Val Lys Arg Leu Leu Ser Phe Gln Arg Tyr Phe His		
333	65 70 75 80		
336	Ala Ser Arg Leu Leu Arg Gly Ile Ile Pro Gln Ala Pro Leu His Leu		
337	85 90 95		
340	Leu Asp Glu Asp Tyr Leu Gly Gln Ala Arg His Met Leu Ser Lys Val		
341	100 105 110		
344	Gly Met Trp Asp Phe Asp Ile Phe Leu Phe Asp Arg Leu Thr Asn Gly		
345	115 120 125		
348	Asn Ser Leu Val Thr Leu Leu Cys His Leu Phe Asn Thr His Gly Leu		
349	130 135 140		
352	Ile His His Phe Lys Leu Asp Met Val Thr Leu His Arg Phe Leu Val		
353	145 150 155 160		
356	Met Val Gln Glu Asp Tyr His Ser Gln Asn Pro Tyr His Asn Ala Val		
357	165 170 175		
360	His Ala Ala Asp Val Thr Gln Ala Met His Cys Tyr Leu Lys Glu Pro		
361	180 185 190		

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364 Lys Leu Ala Ser Phe Leu Thr Pro Leu Asp Ile Met Leu Gly Leu Leu  
 365 195 200 205  
 368 Ala Ala Ala Ala His Asp Val Asp His Pro Gly Val Asn Gln Pro Phe  
 369 210 215 220  
 372 Leu Ile Lys Thr Asn His His Leu Ala Asn Leu Tyr Gln Asn Met Ser  
 373 225 230 235 240  
 376 Val Leu Glu Asn His His Trp Arg Ser Thr Ile Gly Met Leu Arg Glu  
 377 245 250 255  
 380 Ser Arg Leu Leu Ala His Leu Pro Lys Glu Met Thr Gln Asp Ile Glu  
 381 260 265 270  
 384 Gln Gln Leu Gly Ser Leu Ile Leu Ala Thr Asp Ile Asn Arg Gln Asn  
 385 275 280 285  
 388 Glu Phe Leu Thr Arg Leu Lys Ala His Leu His Asn Lys Asp Leu Arg  
 389 290 295 300  
 392 Leu Glu Asp Ala Gln Asp Arg His Phe Met Leu Gln Ile Ala Leu Lys  
 393 305 310 315 320  
 396 Cys Ala Asp Ile Cys Asn Pro Cys Arg Ile Trp Glu Met Ser Lys Gln  
 397 325 330 335  
 400 Trp Ser Glu Arg Val Cys Glu Glu Phe Tyr Arg Gln Gly Glu Leu Glu  
 401 340 345 350  
 404 Gln Lys Phe Glu Leu Glu Ile Ser Pro Leu Cys Asn Gln Gln Lys Asp  
 405 355 360 365  
 408 Ser Ile Pro Ser Ile Gln Ile Gly Phe Met Ser Tyr Ile Val Glu Pro  
 409 370 375 380  
 412 Leu Phe Arg Glu Trp Ala His Phe Thr Gly Asn Ser Thr Leu Ser Glu  
 413 385 390 395 400  
 416 Asn Met Leu Gly His Leu Ala His Asn Lys Ala Gln Trp Lys Ser Leu  
 417 405 410 415  
 420 Leu Pro Arg Gln His Arg Ser Arg Gly Ser Ser Gly Ser Gly Pro Asp  
 421 420 425 430  
 424 His Asp His Ala Gly Gln Gly Thr Glu Ser Glu Glu Gln Glu Gly Asp  
 425 435 440 445  
 428 Ser Pro  
 429 450  
 432 <210> SEQ ID NO: 6  
 433 <211> LENGTH: 1353  
 434 <212> TYPE: DNA  
 435 <213> ORGANISM: Human  
 437 <400> SEQUENCE: 6  
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 442 gaacgcgtt gtccttaccc attcatttgc ttccgcctac ttaacagttt aacatactca 180  
 444 ggggagattt gtcaccaagaa aaagggtgaaa agactattaa gctttcaaaat atacttccat 240  
 446 gcatcaaggc tgcttcgtgg aatttatacca caagccccctc tgccacctgtt ggtatgaagac 300  
 448 taccttggac aagcaaggca tatgtcttcc aaagggtggaa tggggattt tgacattttc 360  
 450 ttgtttgatc gcttgacaaa tggaaacagc ctggtaacac ttgtgtgcca cctcttcaat 420  
 452 acccatggac tcatttacca ttcaagttt gatatggtga ctttacaccg atttttagtc 480  
 454 atggttcaag aagattacca cagccaaaac ccgtatcaca atgctgttca cgcagccgac 540  
 456 gtcacccaggccatgcactt ctacctgaaa gagccaaagc ttgcccagtt ctttacaccg 600

**VERIFICATION SUMMARY**

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